

SEQUENCE LISTING

<110> Martin, Gregory B.  
Abramovitch, Robert B.  
Lin, Nai-Chun  
Kim, Young-Jin

<120> BACTERIAL EFFECTOR PROTEINS WHICH INHIBIT PROGRAMMED  
CELL DEATH

<130> 3213/104

<140> 10/524,750  
<141> 2003-08-13

<150> 60/404,339  
<151> 2002-08-16

<150> 60/425,842  
<151> 2002-11-12

<150> PCT/US03/25247  
<151> 2003-08-16

<160> 54

<170> PatentIn Ver. 2.1

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<211> 1662  
<212> DNA  
<213> *Pseudomonas syringae*

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caggttcagc cgccgaccctc gaataactccc ccgtcgaacg cggccgcacc gcccacaacc 180  
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<211> 553  
<212> PRT  
<213> Pseudomonas syringae

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Gly Ala Ser Ser Ser Asn Ser Pro Gln Val Gln Pro Arg Pro Ser Asn  
35 40 45  
  
Thr Pro Pro Ser Asn Ala Pro Ala Pro Pro Pro Thr Gly Arg Glu Arg  
50 55 60  
  
Leu Ser Arg Ser Thr Ala Leu Ser Arg Gln Thr Arg Glu Trp Leu Glu  
65 70 75 80  
  
Gln Gly Met Pro Thr Ala Glu Asp Ala Ser Val Arg Arg Arg Pro Gln  
85 90 95  
  
Val Thr Ala Asp Ala Ala Thr Pro Arg Ala Glu Ala Arg Arg Thr Pro  
100 105 110  
  
Glu Ala Thr Ala Asp Ala Ser Ala Pro Arg Arg Gly Ala Val Ala His  
115 120 125  
  
Ala Asn Ser Ile Val Gln Gln Leu Val Ser Glu Gly Ala Asp Ile Ser  
130 135 140

His Thr Arg Asn Met Leu Arg Asn Ala Met Asn Gly Asp Ala Val Ala  
145 150 155 160

Phe Ser Arg Val Glu Gln Asn Ile Phe Arg Gln His Phe Pro Asn Met  
165 170 175

Pro Met His Gly Ile Ser Arg Asp Ser Glu Leu Ala Ile Glu Leu Arg  
180 185 190

Gly Ala Leu Arg Arg Ala Val His Gln Gln Ala Ala Ser Ala Pro Val  
195 200 205

Arg Ser Pro Thr Pro Thr Pro Ala Ser Pro Ala Ala Ser Ser Ser Gly  
210 215 220

Ser Ser Gln Arg Ser Leu Phe Gly Arg Phe Ala Arg Leu Met Ala Pro  
225 230 235 240

Asn Gln Gly Arg Ser Ser Asn Thr Ala Ala Ser Gln Thr Pro Val Asp  
245 250 255

Arg Ser Pro Pro Arg Val Asn Gln Arg Pro Ile Arg Val Asp Arg Ala  
260 265 270

Ala Met Arg Asn Arg Gly Asn Asp Glu Ala Asp Ala Ala Leu Arg Gly  
275 280 285

Leu Val Gln Gln Gly Val Asn Leu Glu His Leu Arg Thr Ala Leu Glu  
290 295 300

Arg His Val Met Gln Arg Leu Pro Ile Pro Leu Asp Ile Gly Ser Ala  
305 310 315 320

Leu Gln Asn Val Gly Ile Asn Pro Ser Ile Asp Leu Gly Glu Ser Leu  
325 330 335

Val Gln His Pro Leu Leu Asn Leu Asn Val Ala Leu Asn Arg Met Leu  
340 345 350

Gly Leu Arg Pro Ser Ala Glu Arg Ala Pro Arg Pro Ala Val Pro Val  
355 360 365

Ala Pro Ala Thr Ala Ser Arg Arg Pro Asp Gly Thr Arg Ala Thr Arg  
370 375 380

Leu Arg Val Met Pro Glu Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr  
385 390 395 400

Gly Val Arg Leu Leu Asn Leu Asn Pro Gly Val Gly Val Arg Gln Ala  
405 410 415

Val Ala Ala Phe Val Thr Asp Arg Ala Glu Arg Pro Ala Val Val Ala  
420 425 430

Asn Ile Arg Ala Ala Leu Asp Pro Ile Ala Ser Gln Phe Ser Gln Leu  
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Arg Thr Ile Ser Lys Ala Asp Ala Glu Ser Glu Glu Leu Gly Phe Lys  
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Asp Ala Ala Asp His His Thr Asp Asp Val Thr His Cys Leu Phe Gly  
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Gly Glu Leu Ser Leu Ser Asn Pro Asp Gln Gln Val Ile Gly Leu Ala  
485 490 495

Gly Asn Pro Thr Asp Thr Ser Gln Pro Tyr Ser Gln Glu Gly Asn Lys  
500 505 510

Asp Leu Ala Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly  
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Lys Pro Glu His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile  
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Ala Lys Tyr Ala Phe Arg Ile Val Pro  
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<211> 1740

<212> DNA

<213> Pseudomonas syringae

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acggcggagg ctggagtgcc catcaggccg caggagtctg ccgaggctgc agcgccgcag 300  
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aacaccatga ttgacaatgc catgcgtcgc cacgcgatag ctcttccttc tcgaacagta 540  
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<211> 579

<212> PRT

<213> *Pseudomonas syringae*

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Gly Ala Arg Ser Ser Asn Ser Pro Arg Leu Pro Ala Pro Pro Asp Ala  
35 40 45

Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg  
50 55 60

Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro  
65 70 75 80

Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala  
85 90 95

Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp  
100 105 110

Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala  
115 120 125

Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn  
130 135 140

Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile  
145 150 155 160

Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro  
165 170 175

Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu  
180 185 190

Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala  
195 200 205

Ala Leu Arg Arg Glu Val Arg Gln Gln Glu Ala Ser Ala Pro Pro Arg  
210 215 220

Thr Ala Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro  
225 230 235 240

Pro Thr Ser Thr Glu Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu  
245 250 255

Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser  
260 265 270

Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro  
275 280 285

Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn  
290 295 300

His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln  
305 310 315 320

Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu  
325 330 335

His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val  
340 345 350

Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Asn Pro  
355 360 365

Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro  
370 375 380

Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr  
385 390 395 400

Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile  
405 410 415

Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu  
420 425 430

Leu Ser Leu Asn Pro Gly Ala Gly Val Arg Glu Thr Val Ala Ala Phe  
435 440 445

Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala  
450 455 460

Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys  
465 470 475 480

Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Ala Ala Asp His  
485 490 495

Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr  
500 505 510

Ser Ser Asp Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met  
515 520 525

Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp  
530 535 540

Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu His Pro Met  
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Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr Ala Phe Arg  
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Ile Val Pro

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<212> DNA  
<213> *Pseudomonas syringae*

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<222> (1100)  
<223> N at position 1100 can be A, C, T, or G

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<212> PRT  
<213> *Pseudomonas syringae*

<220>  
<221> UNSURE  
<222> (367)  
<223> Xaa at position 367 can be any amino acid

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Gly Ala Ser Ser Ser Asn Ser Pro Arg Leu Pro Ala Pro Pro Asp Ala  
35 40 45

Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg  
50 55 60

Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro  
65 70 75 80

Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala  
85 90 95

Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp  
100 105 110

Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala  
115 120 125

Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn  
130 135 140

Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile  
145 150 155 160

Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro  
165 170 175

Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu  
180 185 190

Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala  
195 200 205

Ala Leu Arg Arg Glu Val Arg Gln Gln Glu Ala Ser Ala Pro Pro Arg  
210 215 220

Thr Thr Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro  
225 230 235 240

Pro Thr Ser Thr Glu Ser Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu  
245 250 255

Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser  
260 265 270

Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro  
275 280 285

Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn  
290 295 300

His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln  
305 310 315 320

Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu  
325 330 335

His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val  
340 345 350

Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Xaa Pro  
355 360 365

Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro  
370 375 380

Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr  
385 390 395 400

Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile  
405 410 415

Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu  
420 425 430

Leu Ser Leu Asn Pro Gly Ala Trp Val Arg Glu Thr Val Ala Ala Phe  
435 440 445

Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala  
450 455 460

Ala Leu Asn Leu Sér Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys  
465 470 475 480

Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Leu Ala Asp His  
485 490 495

Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr  
500 505 510

Ser Ser Val Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met  
515 520 525

Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp  
530 535 540

Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu His Pro Met  
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Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr Ala Phe Arg  
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Ile Val Pro

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<211> 1740

<212> DNA

<213> Pseudomonas syringae

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<213> Pseudomonas syringae

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Pro Ala Ser Gln Ala Arg Asp Arg Arg Glu Met Leu Leu Arg Ala Arg  
50 55 60  
  
Pro Leu Ser Arg Gln Thr Arg Glu Trp Val Ala Gln Gly Met Pro Pro  
65 70 75 80  
  
Thr Ala Glu Ala Gly Val Pro Ile Arg Pro Gln Glu Ser Ala Glu Ala  
85 90 95  
  
Ala Ala Pro Gln Ala Arg Ala Glu Glu Arg His Thr Pro Glu Ala Asp  
100 105 110  
  
Ala Ala Ala Ser His Val Arg Thr Glu Gly Gly Arg Thr Pro Gln Ala  
115 120 125  
  
Leu Ala Gly Thr Ser Pro Arg His Thr Gly Ala Val Pro His Ala Asn  
130 135 140  
  
Arg Ile Val Gln Gln Leu Val Asp Ala Gly Ala Asp Leu Ala Gly Ile  
145 150 155 160  
  
Asn Thr Met Ile Asp Asn Ala Met Arg Arg His Ala Ile Ala Leu Pro  
165 170 175  
  
Ser Arg Thr Val Gln Ser Ile Leu Ile Glu His Phe Pro His Leu Leu  
180 185 190  
  
Ala Gly Glu Leu Ile Ser Gly Ser Glu Leu Ala Thr Ala Phe Arg Ala

195

200

205

Ala Leu Arg Arg Glu Val Arg Gln Gln Glu Ala Ser Ala Pro Pro Arg  
210 215 220

Thr Ala Ala Arg Ser Ser Val Arg Thr Pro Glu Arg Ser Thr Val Pro  
225 230 235 240

Pro Thr Ser Thr Glu Ser Ser Gly Ser Asn Gln Arg Thr Leu Leu  
245 250 255

Gly Arg Phe Ala Gly Leu Met Thr Pro Asn Gln Arg Arg Pro Ser Ser  
260 265 270

Ala Ser Asn Ala Ser Ala Ser Gln Arg Pro Val Asp Arg Ser Pro Pro  
275 280 285

Arg Val Asn Gln Val Pro Thr Gly Ala Asn Arg Val Val Met Arg Asn  
290 295 300

His Gly Asn Asn Glu Ala Asp Ala Ala Leu Gln Gly Leu Ala Gln Gln  
305 310 315 320

Gly Val Asp Met Glu Asp Leu Arg Ala Ala Leu Glu Arg His Ile Leu  
325 330 335

His Arg Arg Pro Ile Pro Met Asp Ile Ala Tyr Ala Leu Gln Gly Val  
340 345 350

Gly Ile Ala Pro Ser Ile Asp Thr Gly Glu Ser Leu Met Glu Asn Pro  
355 360 365

Leu Met Asn Leu Ser Val Ala Leu His Arg Ala Leu Gly Pro Arg Pro  
370 375 380

Ala Arg Ala Gln Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr  
385 390 395 400

Val Ser Arg Arg Pro Asp Ser Ala Arg Ala Thr Arg Leu Gln Val Ile  
405 410 415

Pro Ala Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu  
420 425 430

Leu Ser Leu Asn Pro Gly Ala Gly Val Arg Glu Thr Val Ala Ala Phe  
435 440 445

Val Asn Asn Arg Tyr Glu Arg Gln Ala Val Val Ala Asp Ile Arg Ala

450

455

460

Ala Leu Asn Leu Ser Lys Gln Phe Asn Lys Leu Arg Thr Val Ser Lys  
465 470 475 480

Ala Asp Ala Ala Ser Asn Lys Pro Gly Phe Lys Asp Leu Ala Asp His  
485 490 495

Pro Asp Asp Ala Thr Gln Cys Leu Phe Gly Glu Glu Leu Ser Leu Thr  
500 505 510

Ser Ser Val Gln Gln Val Ile Gly Leu Ala Gly Lys Ala Thr Asp Met  
515 520 525

Ser Glu Ser Tyr Ser Arg Glu Ala Asn Lys Asp Leu Val Phe Met Asp  
530 535 540

Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu His Pro Met  
545 550 555 560

Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr Ala Phe Arg  
565 570 575

Ile Val Pro

<210> 9  
<211> 16  
<212> PRT  
<213> Pseudomonas syringae

<400> 9  
Ala Gly Pro Ser Gly Ala Tyr Phe Val Gly His Thr Asp Pro Glu Pro  
1 5 10 15

<210> 10  
<211> 9  
<212> PRT  
<213> Pseudomonas syringae

<400> 10  
Ser Gly Ala Ser Ser Ser Asn Ser Pro  
1 5

<210> 11

<211> 8  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 11  
Leu Ser Arg Gln Thr Arg Glu Trp  
1 5

<210> 12  
<211> 6  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 12  
Ile Val Gln Gln Leu Val  
1 5

<210> 13  
<211> 5  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 13  
Ser Ser Ser Gly Ser  
1 5

<210> 14  
<211> 11  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 14  
Pro Val Asp Arg Ser Pro Pro Arg Val Asn Gln  
1 5 10

<210> 15  
<211> 12  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 15  
Ala Pro Arg Pro Ala Val Pro Val Ala Pro Ala Thr  
1 5 10

<210> 16  
<211> 5  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 16  
Ser Arg Arg Pro Asp  
1 5

<210> 17  
<211> 5  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 17  
Arg Ala Thr Arg Leu  
1 5

<210> 18  
<211> 15  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 18  
Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr Gly Val Arg Leu Leu  
1 5 10 15

<210> 19  
<211> 5  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 19  
Val Ala Ala Phe Val  
1 5

<210> 20  
<211> 5  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 20  
Ile Arg Ala Ala Leu

<210> 21  
<211> 5  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 21  
Ser Lys Ala Asp Ala  
1 5

<210> 22  
<211> 8  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 22  
Gln Gln Val Ile Gly Leu Ala Gly  
1 5

<210> 23  
<211> 38  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 23  
Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly Lys Pro Glu  
1 5 10 15

His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile Ala Lys Tyr  
20 25 30

Ala Phe Arg Ile Val Pro  
35

<210> 24  
<211> 553  
<212> PRT  
<213> *Pseudomonas syringae*

<220>  
<221> UNSURE  
<222> (1)...(6)  
<223> Xaa at positions 1-6 can be any amino acid

<220>  
<221> UNSURE  
<222> (23)..(31)  
<223> Xaa at positions 23-31 can be any amino acid

<220>  
<221> UNSURE  
<222> (41)..(70)  
<223> Xaa at positions 41-70 can be any amino acid

<220>  
<221> UNSURE  
<222> (79)..(131)  
<223> Xaa at positions 79-131 can be any amino acid

<220>  
<221> UNSURE  
<222> (138)..(220)  
<223> Xaa at positions 138-220 can be any amino acid

<220>  
<221> UNSURE  
<222> (226)..(253)  
<223> Xaa at positions 226-253 can be any amino acid

<220>  
<221> UNSURE  
<222> (265)..(360)  
<223> Xaa at positions 265-360 can be any amino acid

<220>  
<221> UNSURE  
<222> (373)  
<223> Xaa at position 373 can be any amino acid

<220>  
<221> UNSURE  
<222> (379)..(380)  
<223> Xaa at positions 379-380 can be any amino acid

<220>  
<221> UNSURE  
<222> (386)..(390)  
<223> Xaa at positions 386-390 can be any amino acid

<220>  
<221> UNSURE

<222> (406)..(433)

<223> Xaa at positions 406-433 can be any amino acid

<220>

<221> UNSURE

<222> (439)..(451)

<223> Xaa at positions 439-451 can be any amino acid

<220>

<221> UNSURE

<222> (457)..(489)

<223> Xaa at positions 457-489 can be any amino acid

<220>

<221> UNSURE

<222> (498)..(515)

<223> Xaa at positions 498-515 can be any amino acid

<400> 24

Xaa Xaa Xaa Xaa Xaa Xaa Ala Gly Pro Ser Gly Ala Tyr Phe Val Gly  
1 5 10 15

His Thr Asp Pro Glu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser  
20 25 30

Gly Ala Ser Ser Ser Asn Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa  
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Leu Ser Arg Gln Thr Arg Glu Trp Xaa Xaa  
65 70 75 80

Xaa  
85 90 95

Xaa  
100 105 110

Xaa  
115 120 125

Xaa Xaa Xaa Ile Val Gln Gln Leu Val Xaa Xaa Xaa Xaa Xaa Xaa  
130 135 140

Xaa  
145 150 155 160

Xaa  
165 170 175

Xaa  
180 185 190

Xaa  
195 200 205

Xaa Ser Ser Ser Gly  
210 215 220

Ser Xaa  
225 230 235 240

Xaa Pro Val Asp  
245 250 255

Arg Ser Pro Pro Arg Val Asn Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
260 265 270

Xaa  
275 280 285

Xaa  
290 295 300

Xaa  
305 310 315 320

Xaa  
325 330 335

Xaa  
340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Ala Pro Arg Pro Ala Val Pro Val  
355 360 365

Ala Pro Ala Thr Xaa Ser Arg Arg Pro Asp Xaa Xaa Arg Ala Thr Arg  
370 375 380

Leu Xaa Xaa Xaa Xaa Xaa Arg Glu Asp Tyr Glu Asn Asn Val Ala Tyr  
385 390 395 400

Gly Val Arg Leu Leu Xaa  
405 410 415

Val Ala Ala Phe Val Xaa  
420 425 430

Xaa Ile Arg Ala Ala Leu Xaa  
435 440 445

Xaa Xaa Xaa Ser Lys Ala Asp Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
450 455 460

Xaa  
465 470 475 480

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Val Ile Gly Leu Ala  
485 490 495

Gly Xaa  
500 505 510

Xaa Xaa Xaa Phe Met Asp Met Lys Lys Leu Ala Gln Phe Leu Ala Gly  
515 520 525

Lys Pro Glu His Pro Met Thr Arg Glu Thr Leu Asn Ala Glu Asn Ile  
530 535 540

Ala Lys Tyr Ala Phe Arg Ile Val Pro  
545 550

<210> 25  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 25  
gtaatgcagc gcctccatat c 21

<210> 26  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 26  
tcaggggact attctaaaag c 21

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 27  
atggcggta tcaatagagc g 21

<210> 28  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 28  
tcacacccgc aatcggttg cac 23

<210> 29  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 29  
tcatacatgt ctttcaaggg ccg 23

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 30  
gtatcaatag agcgggacca tc 22

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 31  
cactgaccac ttgctgaacg 20

<210> 32  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 32  
tgtcgcgcca aaccaggcg tg 22

<210> 33  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 33  
ccatcaccag ggcaaacc 18

<210> 34  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 34  
gtatcgttca gcaattggtc agtg 24

<210> 35  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 35  
acgcgtatgg gtctttggtt g 21

<210> 36  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 36  
acgattgcgg gtgatgc 17

<210> 37  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 37  
cctcttggct gtaaggctgc 20

<210> 38  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 38  
atggcgggta tcaatagagc gg 22

<210> 39  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 39  
gaattcgata tcaagcttat cgataccgtc gacctcgag 39

<210> 40  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 40  
gaattcgaat tgggatatca agtttatcga taccgtcgac ctcgag 46

<210> 41  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 41  
gaattcgaat tgatatcaag ctatcgata ccgtcgacct cgag 44

<210> 42  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 42  
cgaggcgaa cagccgagca g 21

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 43  
gcaattcgaa gtggcagtga 20

<210> 44  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 44  
ttatgcttta ttggtattt tagagg 26

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 45  
atggcggta tcaatagagc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Pseudomonas syringae

<220>  
<221> unsure

<222> (7)..(22)  
<223> N at positions 7-22 can be A, C, T, or G

<400> 46  
ggaactnnnn nnnnnnnnnn nnccac

26

<210> 47  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 47  
Met Ala Gly Ile Asn Arg Ala Gly  
1 5

<210> 48  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence

<220>  
<221> UNSURE  
<222> (2)  
<223> Xaa at position 2 can be any amino acid except E

<220>  
<221> UNSURE  
<222> (3)  
<223> Xaa at position 3 can be any amino acid except D

<220>  
<221> UNSURE  
<222> (4)  
<223> Xaa at position 4 can be any amino acid except R

<220>  
<221> UNSURE  
<222> (5)  
<223> Xaa at position 5 can be any amino acid except K

<220>  
<221> UNSURE  
<222> (6)  
<223> Xaa at position 6 can be any amino acid except H

<220>  
<221> UNSURE  
<222> (7)  
<223> Xaa at position 7 can be any amino acid except P

<220>  
<221> UNSURE  
<222> (8)  
<223> Xaa at position 8 can be any amino acid except F

<220>  
<221> UNSURE  
<222> (9)  
<223> Xaa at position 9 can be any amino acid except Y

<220>  
<221> UNSURE  
<222> (10)  
<223> Xaa at position 10 can be any amino acid except W

<220>  
<221> UNSURE  
<222> (11)..(12)  
<223> Xaa at positions 11-12 can be any amino acid

<220>  
<221> UNSURE  
<222> (19)  
<223> Xaa at position 19 can be any amino acid except P

<400> 48  
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Thr Ala Gly  
1 5 10 15

Cys Asn Xaa

<210> 49  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus sequence

<220>  
<221> UNSURE  
<222> (2)..(3)  
<223> Xaa at positions 2-3 can be any amino acid

<220>  
<221> UNSURE  
<222> (5)..(6)  
<223> Xaa at positions 5-6 can be any amino acid

<220>  
<221> UNSURE  
<222> (8)..(9)  
<223> Xaa at positions 8-9 can be any amino acid

<220>  
<221> UNSURE  
<222> (11)  
<223> Xaa at position 11 can be any amino acid

<220>  
<221> UNSURE  
<222> (13)..(15)  
<223> Xaa at positions 13-15 can be any amino acid

<400> 49  
Arg Xaa Xaa Leu Xaa Xaa Ser Xaa Xaa Leu Xaa Arg Xaa Xaa Xaa Glu  
1 5 10 15

<210> 50  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus sequence

<220>  
<221> UNSURE  
<222> (2)  
<223> Xaa at position 2 can be any amino acid

<220>  
<221> UNSURE  
<222> (4)  
<223> Xaa at position 4 can be any amino acid

<400> 50  
Ser Xaa Arg Xaa Arg  
1 5

<210> 51  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence

<220>  
<221> UNSURE  
<222> (4)..(8)  
<223> Xaa at positions 4-8 can be any amino acid

<400> 51  
Asn Pro Ser Xaa Xaa Xaa Xaa Xaa Ser  
1 5

<210> 52  
<211> 539  
<212> PRT  
<213> Pseudomonas syringae

<400> 52  
Met Pro Gly Ile Asn Gly Ala Gly Pro Ser Asn Phe Phe Trp Gln Trp  
1 5 10 15

Arg Thr Asp Gly Glu Pro Val Thr Glu Arg Glu His Asp Ser Ser Arg  
20 25 30

Ser Ala Ser Ser Ala Asn Ser Pro Glu Leu Pro Pro Pro Ala Ser Pro  
35 40 45

Ala Glu Ser Gly Arg Gln Arg Leu Leu Arg Ser Ser Ala Leu Ser Arg  
50 55 60

Gln Thr Arg Glu Trp Leu Glu Ala Thr Pro Ala Arg Val Gln Gly Ala  
65 70 75 80

Thr Pro Pro Ala Glu Ala Arg Gln Ser Pro Glu Ala Gln Gln Ala Glu  
85 90 95

Arg Ile Val Gln Glu Leu Val Arg Gly Gly Ala Asp Leu Asn Asn Val  
100 105 110

Arg Thr Met Leu Arg Asn Val Met Asp Asn Asn Ala Val Ala Phe Ser  
115 120 125

Arg Val Glu Arg Asp Ile Leu Leu Gln His Phe Pro Asn Met Pro Met  
130 135 140

Thr Gly Ile Ser Ser Asp Ser Val Leu Ala Asn Glu Leu Arg Gln Arg  
145 150 155 160

Leu Arg Gln Thr Val Arg Gln Gln Arg Ile Gln Ser Ser Thr Pro Ala  
165 170 175

Arg Leu Ala Asp Ser Ser Gly Ser Ser Gln Arg Ser Leu Ile Gly  
180 185 190

Arg Ser Thr Met Leu Met Thr Pro Gly Arg Ser Ser Ser Ser Ala  
195 200 205

Ala Ala Ser Arg Thr Ser Val Asp Arg His Pro Gln Gly Leu Asp Leu  
210 215 220

Glu Ser Ala Arg Leu Ala Ser Ala Ala Arg His Asn His Ser Ala Asn  
225 230 235 240

Gln Thr Asn Glu Ala Leu Arg Arg Leu Thr Gln Glu Gly Val Asp Met  
245 250 255

Glu Arg Leu Arg Thr Ser Leu Gly Arg Tyr Ile Met Ser Leu Glu Pro  
260 265 270

Leu Pro Pro Asp Leu Arg Arg Ala Leu Glu Ser Val Gly Ile Asn Pro  
275 280 285

Phe Ile Pro Glu Glu Leu Ser Leu Val Asp His Pro Val Leu Asn Phe  
290 295 300

Ser Ala Ala Leu Asn Arg Met Leu Ala Ser Arg Gln Thr Thr Thr Asn  
305 310 315 320

Ser Pro Glu Leu Pro Pro Leu Ala Ser Ser Ala Glu Ser Gly Arg Arg  
325 330 335

Arg Leu Leu Arg Ser Pro Pro Leu Leu Ser Gly Gln Arg Glu Trp Ile  
340 345 350

Glu Gln Ser Met Arg Gln Glu Ala Glu Pro Gln Ser Ser Arg Leu Asn  
355 360 365

Arg Ala Val Arg Leu Ala Val Met Pro Pro Gln Asn Glu Asn Glu Asp  
370 375 380

Asn Val Ala Tyr Ala Ile Arg Leu Arg Arg Leu Asn Pro Gly Ala Asp  
385 390 395 400

Val Ser Arg Val Val Ala Ser Phe Ile Thr Asp Pro Ala Ala Arg Gln  
405 410 415

Gln Val Val Asn Asp Ile Arg Ala Ala Leu Asp Ile Ala Pro Gln Phe  
420 425 430

Ser Gln Leu Arg Thr Ile Ser Lys Ala Asp Ala Glu Ser Glu Glu Leu  
435 440 445

Gly Phe Arg Asp Ala Ala Asp His Pro Asp Asn Ala Thr Ser Cys Leu  
450 455 460

Phe Gly Glu Glu Leu Ser Leu Ser Asn Pro Asp Gln Gln Val Ile Gly  
465 470 475 480

Leu Ala Val Asn Pro Thr Asp Lys Pro Gln Pro Tyr Ser Gln Glu Val  
485 490 495

Asn Lys Ala Leu Thr Phe Met Asp Met Lys Lys Leu Ala Gln Tyr Leu  
500 505 510

Ala Asp Lys Pro Glu His Pro Leu Asn Arg Gln Arg Leu Asp Ala Lys  
515 520 525

Asn Ile Ala Lys Tyr Ala Phe Lys Ile Val Pro  
530 535

<210> 53  
<211> 158  
<212> PRT  
<213> *Pseudomonas syringae*

<400> 53

Met Gly Asn Ile Cys Val Gly Gly Ser Arg Met Ala His Gln Val Asn  
1 5 10 15

Ser Pro Asp Arg Val Ser Asn Asn Ser Gly Asp Glu Asp Asn Val Thr  
20 25 30

Ser Ser Gln Leu Leu Ser Val Arg His Gln Leu Ala Glu Ser Ala Gly  
35 40 45

Leu Pro Arg Asp Gln His Glu Phe Val Ser Ser Gln Ala Pro Gln Ser  
50 55 60

Leu Arg Asn Arg Tyr Asn Asn Leu Tyr Ser His Thr Gln Arg Thr Leu  
65 70 75 80

Asp Met Ala Asp Met Gln His Arg Tyr Met Thr Gly Ala Ser Gly Ile  
85 90 95

Asn Pro Gly Met Leu Pro His Glu Asn Val Asp Asp Met Arg Ser Ala  
100 105 110

Ile Thr Asp Trp Ser Asp Met Arg Glu Ala Leu Gln His Ala Met Gly  
115 120 125

Ile His Ala Asp Ile Pro Pro Ser Pro Glu Arg Phe Val Ala Thr Met  
130 135 140

Asn Pro Ser Gly Ser Ile Arg Met Ser Thr Leu Ser Pro Ser  
145 150 155

<210> 54

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus  
sequence

<220>

<221> UNSURE

<222> (2)

<223> Xaa at position 2 can be any amino acid

<220>

<221> UNSURE

<222> (4)..(5)

<223> Xaa at positions 4-5 can be any amino acid

<220>

<221> UNSURE

<222> (7)..(8)

<223> Xaa at positions 7-8 can be any amino acid

<220>

<221> UNSURE

<222> (10)..(11)

<223> Xaa at positions 10-11 can be any amino acid

<220>

<221> UNSURE

<222> (13)

<223> Xaa at position 13 can be any amino acid

<220>

<221> UNSURE

<222> (15)..(17)

<223> Xaa at positions 15-17 can be any amino acid

<400> 54

Ser Xaa Arg Xaa Xaa Leu Xaa Xaa Ser Xaa Xaa Leu Xaa Arg Xaa Xaa

1

5

10

15

Xaa Glu